

SEQUENCE LISTING

<110> Rosen, Craig A.
Haseltine, William A.

<120> Albumin Fusion Proteins

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<141> 2001-04-12

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<170> PatentIn Ver. 2.1

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 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

cgt gaa acc tat ggt gaa atg gtc gac tgc tgt gca aaa caa gaa cct 288
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Ala Lys Gln Glu Pro
 85 90 95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

ccc cga ttg gtc aga cca gag gtt gat gtc act gct ttt cat 384
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga	432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg	
130 135 140	
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg	
145 150 155 160	
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala	
165 170 175	
tgc ctg ttg cca aag ctc gat gaa ctt ccg gat gaa ggg aag gct tcg	576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser	
180 185 190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu	
195 200 205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga att ccc	672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro	
210 215 220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys	
225 230 235 240	
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp	
245 250 255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser	
260 265 270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His	
275 280 285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser	
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tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala	
305 310 315 320	
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg	
325 330 335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr	
340 345 350	
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu	
355 360 365	

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag gct Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro 370 375 380	1152
cag aat tta atc aaa caa aac tgc ttt gag cag ctt gga gag Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu 385 390 395 400	1200
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro 405 410 415	1248
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys 420 425 430	1296
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys 435 440 445	1344
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His 450 455 460	1392
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser 465 470 475 480	1440
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr 485 490 495	1488
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp 500 505 510	1536
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala 515 520 525	1584
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu 530 535 540	1632
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys 545 550 555 560	1680
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val 565 570 575	1728
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<213> Homo Sapiens

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
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Tyr Ser Arg Ser Leu Asp Lys Arg
      20

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albumin fusion VECTOR

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<222> (5)..(10)
<223> BamHI restriction site

<220>
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<222> (11)..(16)
<223> Hind III restriction site

<220>
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<222> (17)..(27)
<223> Kozak sequence
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<222> (25)...(97)
<223> cds natural signal sequence of human serum albumin

<220>
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<223> XhoI restriction site

<220>
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<222> (98)...(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcaggatcc aagttccgc caccatgaag tggtaacct ttatccctc tcttttctc 60
tttagctcg cttactcgag gggtgtgtt cgtcgagatg cacacaagag tgag      114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
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<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<222> (6)...(11)
<223> Asp718 restriction site

<220>
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<222> (12)...(17)
<223> EcoRI restriction site

<220>
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<222> (15)...(17)
<223> reverse complement of stop codon

<220>
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<222> (18)...(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)...(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc ggcgcctata agcctaaggc agc      43
<210> 32
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<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<222> forward primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>
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<220>
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<222> (46)
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<400> 32
ccggcgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
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<223> reverse primer useful for inserting Therapeutic protein into pC4:HSa vector

<220>
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<210> 34

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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<223> Stanniocalcin signal peptide

<400> 34

Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 35

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> signal

<223> Synthetic signal peptide

<400> 35

Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 36

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 36
caggtgcagc tgggtgcagtc tgg

23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 37
caggtcaact taagggagtc tgg

23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate VH forward primer useful for
amplifying human VH domains

<400> 38
gaggtgcagc tgggtggagtc tgg

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<210> 39
<211> 23
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<220>
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<400> 39
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<210> 40
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<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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<400> 40
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<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VH domains

<400> 41
cagggtacagc tgcagcgttc agg

23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc

24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc

24

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc

24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

24

<220>
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amplifying human VH domains

<400> 45
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<210> 46
<211> 23
<212> DNA
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<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 46
gacatccaga tgacccagtc tcc 23

<210> 47
<211> 23
<212> DNA
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<220>
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<223>Degenerate Vkappa forward primer useful for
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<400> 47
gatgttgtga tgactcagtc tcc 23

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 48
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<210> 49
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<400> 49
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<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 50
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<210> 51
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<400> 51
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<210> 52
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<213> Artificial Sequence

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<400> 52
gaaattgtgc tgactcagtc tcc 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc 23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 54
cagtcgtccc tgactcagcc tgc 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 55
tccttatgtgc tgactcagcc acc 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Vlambda forward primer useful for amplifying human VL domains

<400> 56
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<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

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<400> 57
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<210> 58
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<212> DNA
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<400> 58
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<210> 59
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amplifying human VL domains		
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amplifying human VL domains		
<400> 62		
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<210> 63		
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amplifying human VL domains		

<400> 63	
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<210> 64	
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amplifying human VL domains	
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amplifying human VL domains	
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amplifying human VL domains	
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amplifying human VL domains

<400> 68
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23

<210> 69
<211> 23
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<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 69
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23

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 70
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23

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 71
aattttatgc tgactcagcc cca

23

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221>turn
<223>Linker peptide that may be used to join VH
and VL domains in an scFv.

<400> 72
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15